

0570
1108

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RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/973,322

DATE: 10/30/2001

TIME: 15:33:49

Input Set : A:\SEQLISTDYOU17001CP1.TXT

Output Set : N:\CRF3\10302001\I973322.raw

ENTERED

#2

```

4 <110> APPLICANT: Hope, Ralph Graham
5      McLauchlan, John
7 <120> TITLE OF INVENTION: VIRAL THERAPEUTICS
10 <130> FILE REFERENCE: DYOU17.001CP1
C--> 12 <140> CURRENT APPLICATION NUMBER: US/09/973,322
C--> 12 <141> CURRENT FILING DATE: 2001-10-09
12 <150> PRIOR APPLICATION NUMBER: US 09/201,916
13 <151> PRIOR FILING DATE: 1998-12-01
15 <150> PRIOR APPLICATION NUMBER: GB 9825951.8
16 <151> PRIOR FILING DATE: 1998-11-26
18 <160> NUMBER OF SEQ ID NOS: 20
20 <170> SOFTWARE: FastSEQ for Windows Version 4.0
22 <210> SEQ ID NO: 1
23 <211> LENGTH: 630
24 <212> TYPE: DNA
25 <213> ORGANISM: Hepatitis C Virus
27 <220> FEATURE:
28 <221> NAME/KEY: CDS
29 <222> LOCATION: (43)...(630)
31 <400> SEQUENCE: 1
32 ggtgcttgcg agtgcccgagggtctcgtagaccgtgca cc atg agc acg aat      54
33                                     Met Ser Thr Asn
34                                     1
36 cct aaa cct caa aga aaa acc aaa cgt aac acc aac cgt cgc cca cag      102
37 Pro Lys Pro Gln Arg Lys Thr Lys Arg Asn Thr Asn Arg Arg Pro Gln
38 5                                     10                                     15                                     20
40 gac gtt aag ttc ccg ggt ggc ggt cag atc gtt ggt gga gtt tac ttg      150
41 Asp Val Lys Phe Pro Gly Gly Gly Gln Ile Val Gly Gly Val Tyr Leu
42                                     25                                     30                                     35
44 ttg ccg cgc agg ggc cct aga ttg ggt gtg cgc gcg acg agg aag act      198
45 Leu Pro Arg Arg Gly Pro Arg Leu Gly Val Arg Ala Thr Arg Lys Thr
46                                     40                                     45                                     50
48 tcc gag cgg tcg caa cct cga ggt aga cgt cag cct atc ccc aag gca      246
49 Ser Glu Arg Ser Gln Pro Arg Gly Arg Arg Gln Pro Ile Pro Lys Ala
50                                     55                                     60                                     65
52 cgt cgg ccc aag ggc agg aac tgg gct cag ccc ggg tat cct tgg ccc      294
53 Arg Arg Pro Lys Gly Arg Asn Trp Ala Gln Pro Gly Tyr Pro Trp Pro
54                                     70                                     75                                     80
56 ctc tat ggc aat gag ggt tgc ggg tgg gcg gga tgg ctc ctg tcc ccc      342
57 Leu Tyr Gly Asn Glu Gly Cys Gly Trp Ala Gly Trp Leu Leu Ser Pro
58 85                                     90                                     95                                     100
60 agt ggc tct cgg cct agt tgg ggc ccc aac gac ccc cga cgt agg tcg      390
61 Ser Gly Ser Arg Pro Ser Trp Gly Pro Asn Asp Pro Arg Arg Arg Ser
62                                     105                                     110                                     115
64 cgc aat ttg ggt aag gtc atc gat acc ctt acg tgc ggc ttc gtc gat      438
65 Arg Asn Leu Gly Lys Val Ile Asp Thr Leu Thr Cys Gly Phe Val Asp
66                                     120                                     125                                     130

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```

68 ctc atg ggg tac ata ccg ctc gtc ggc gcc cct ctt aga ggc gct gcc 486
69 Leu Met Gly Tyr Ile Pro Leu Val Gly Ala Pro Leu Arg Gly Ala Ala
70      135      140      145
72 agg gcc ctg gcg cat ggc gtc cgg gtt ctg gaa gac ggt gtg aac tat 534
73 Arg Ala Leu Ala His Gly Val Arg Val Leu Glu Asp Gly Val Asn Tyr
74      150      155      160
76 gca aca ggt aac ctt cct ggt tgc tct ttc tct atc ttc ctt ctg gcc 582
77 Ala Thr Gly Asn Leu Pro Gly Cys Ser Phe Ser Ile Phe Leu Leu Ala
78 165      170      175      180
80 ctg ctc tct tgc ctg act gtg ccc gct tca gcc tac caa gtg cgc aac 630
81 Leu Leu Ser Cys Leu Thr Val Pro Ala Ser Ala Tyr Gln Val Arg Asn
82      185      190      195
86 <210> SEQ ID NO: 2
87 <211> LENGTH: 60
88 <212> TYPE: DNA
89 <213> ORGANISM: Hepatitis C Virus
91 <220> FEATURE:
92 <221> NAME/KEY: CDS
93 <222> LOCATION: (1)...(60)
94 <223> OTHER INFORMATION: Corresponds to aa 125 to 144 of SEQ ID. No. 1
96 <400> SEQUENCE: 2
97 acc ctt acg tgc ggc ttc gtc gat ctc atg ggg tac ata ccg ctc gtc 48
98 Thr Leu Thr Cys Gly Phe Val Asp Leu Met Gly Tyr Ile Pro Leu Val
99 1      5      10      15
101 ggc gcc cct ctt 60
102 Gly Ala Pro Leu
103      20
106 <210> SEQ ID NO: 3
107 <211> LENGTH: 18
108 <212> TYPE: DNA
109 <213> ORGANISM: Hepatitis C Virus
111 <220> FEATURE:
112 <221> NAME/KEY: CDS
113 <222> LOCATION: (1)...(18)
114 <223> OTHER INFORMATION: Corresponds to aa 161-166 of SEQ ID. No. 1
116 <400> SEQUENCE: 3
117 ggt gtg aac tat gca aca 18
118 Gly Val Asn Tyr Ala Thr
119 1      5
122 <210> SEQ ID NO: 4
123 <211> LENGTH: 1900
124 <212> TYPE: DNA
125 <213> ORGANISM: Human
127 <220> FEATURE:
128 <221> NAME/KEY: misc_feature
129 <222> LOCATION: (1)...(1900)
130 <223> OTHER INFORMATION: n = A,T,C or G
132 <400> SEQUENCE: 4
133 cgtcttcggg acgcgccgc tcttcgcctt tcgctgcagt ccgtcgattt cttttccag 60

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```

134 gaagaaaaat ggcataccgtt gcagttgata cacaaccgag tgtggtgact cgggtggtca 120
135 acctgccctt ggtgagctcc acgtatgacc tcatgtcctc agcctatctc agtacaaagg 180
136 accagtatcc ctacctgaag tctgtgtgtg agatgscaga gaacggtgtg aagaccatca 240
137 cctccgtggc catgaccagt gctctgcccc tcatccagaa gctagagccg caaattgcag 300
138 ttgccgatac ctatgcctgt aaggggctag acaggattga ggagagactg cctattctga 360
139 atcagccatc aactcagatt gttgccaatg ccaaaggcgc tgtgactggg gcaaaagatg 420
W--> 140 ctgtgacgac tactgtgact ggggccaagg attctgtngc cagcacgac acaggggtga 480
141 tggacaagac caaaggggca gtgactggca gtgtggagaa gaccaagtct gtggtcagt 540
142 gcagcattaa cacagtcttg gggagtcgga tgatgcagct cgtgagcagt ggcgtagaaa 600
143 atgcactcac caaatcagag ctgttggtag aacagtacct ccctctcact gaggaagaac 660
144 tagaaaaaga agcaaaaaaa gttgaaggat ttgatctggt tcagaagcca agttattatg 720
145 ttagactggg atccctgtct accaagcttc actcccgctc ctaccagcag gctctcagca 780
146 gggttaaaaga agctaagcaa aaaagccaac agaccatttc tcagctccat tctactgttc 840
147 acctgattga atttgccagg aagaatgtgt atagtgccaa tcagaaaatt caggatgtct 900
148 aggataagct ctacctctca tgggtagagt ggaaaaggag cattggatat gatgatactg 960
149 atgagtccca ctgtgctgag cacattgagt cactactct tgcaattgcc cgcaacctga 1020
150 ctccagcagc ccagaccagc tgccacaccc tcctgtccaa catccaaggt gtaccacaga 1080
151 acatccaaga tcaagccaag cacatggggg tgatggcagg cgacatctac tcagtgttcc 1140
152 gcaatgctgc ctcttttaaa gaagtgtctg acagcctcct cacttctagc aaggggcagc 1200
153 tgcagaaaat gaaggaatct ttagatgacg tgatggatta tcttgtaaac aacacgcccc 1260
154 tcaactggct ggtaggtccc ttttatcctc agctgactga gtctcagaat gctcaggacc 1320
155 aaggtgcaga gatggacaag agcagccagg agaccagcg atctgagcat aaaactcatt 1380
156 aaacctgccc ctatcactag tgcatgctgt ggccagacag atgacacctt ttgttatgtt 1440
157 gaaattaact tgctaggcaa ccctaaattg ggaagcaagt agctagtata aaggccctca 1500
158 attgtagtgt tttccagctg aattaagagc tttaaagttt ctggcattag cagatgattt 1560
159 ctgttcacct ggtaagaaaa gaatgatagg cttgtcagag cctatagcca gaactcagaa 1620
160 aaaattcaaa tgcacttatg ttctcattct atggccattg tgttgccctc gttactgttt 1680
161 gtattgaata aaaacatctt catgtgggct ggggtagaaa ctgggtgtctg ctctgggtgtg 1740
162 atctgaaaag gcgtcttcac tgctttatct catgatgctt gcttgtaaaa cttgatttta 1800
163 gtttttcatt tctcaaatag gaatactacc tttgaattca ataaaattca ctgcaggata 1860
W--> 164 gaccagttna gnageaaaca nncangtaca cnaaganac 1900
166 <210> SEQ ID NO: 5
167 <211> LENGTH: 437
168 <212> TYPE: PRT
169 <213> ORGANISM: Human
171 <220> FEATURE:
172 <221> NAME/KEY: VARIANT
173 <222> LOCATION: (1)...(437)
174 <223> OTHER INFORMATION: Xaa = Any Amino Acid
176 <400> SEQUENCE: 5
177 Met Ala Ser Val Ala Val Asp Pro Gln Pro Ser Val Val Thr Arg Val
178 1 5 10 15
179 Val Asn Leu Pro Leu Val Ser Ser Thr Tyr Asp Leu Met Ser Ser Ala
180 20 25 30
181 Tyr Leu Ser Thr Lys Asp Gln Tyr Pro Tyr Leu Lys Ser Val Cys Glu
182 35 40 45
W--> 183 Met Xaa Glu Asn Gly Val Lys Thr Ile Thr Ser Val Ala Met Thr Ser
184 50 55 60
185 Ala Leu Pro Ile Ile Gln Lys Leu Glu Pro Gln Ile Ala Val Ala Asp

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```

186 65          70          75          80
187 Thr Tyr Ala Cys Lys Gly Leu Asp Arg Ile Glu Glu Arg Leu Pro Ile
188          85          90          95
189 Leu Asn Gln Pro Ser Thr Gln Ile Val Ala Asn Ala Lys Gly Ala Val
190          100          105          110
191 Thr Gly Ala Lys Asp Ala Val Thr Thr Thr Val Thr Gly Ala Lys Asp
192          115          120          125
193 Ser Val Ala Ser Thr Ile Thr Gly Val Met Asp Lys Thr Lys Gly Ala
194          130          135          140
195 Val Thr Gly Ser Val Glu Lys Thr Lys Ser Val Val Ser Gly Ser Ile
196 145          150          155          160
197 Asn Thr Val Leu Gly Ser Arg Met Met Gln Leu Val Ser Ser Gly Val
198          165          170          175
199 Glu Asn Ala Leu Thr Lys Ser Glu Leu Leu Val Glu Gln Tyr Leu Pro
200          180          185          190
201 Leu Thr Glu Glu Glu Leu Glu Lys Glu Ala Lys Lys Val Glu Gly Phe
202          195          200          205
203 Asp Leu Val Gln Lys Pro Ser Tyr Tyr Val Arg Leu Gly Ser Leu Ser
204          210          215          220
205 Thr Lys Leu His Ser Arg Ala Tyr Gln Gln Ala Leu Ser Arg Val Lys
206 225          230          235          240
207 Glu Ala Lys Gln Lys Ser Gln Gln Thr Ile Ser Gln Leu His Ser Thr
208          245          250          255
209 Val His Leu Ile Glu Phe Ala Arg Lys Asn Val Tyr Ser Ala Asn Gln
210          260          265          270
211 Lys Ile Gln Asp Ala Gln Asp Lys Leu Tyr Leu Ser Trp Val Glu Trp
212          275          280          285
213 Lys Arg Ser Ile Gly Tyr Asp Asp Thr Asp Glu Ser His Cys Ala Glu
214          290          295          300
215 His Ile Glu Ser Arg Thr Leu Ala Ile Ala Arg Asn Leu Thr Gln Gln
216 305          310          315          320
217 Leu Gln Thr Thr Cys His Thr Leu Leu Ser Asn Ile Gln Gly Val Pro
218          325          330          335
219 Gln Asn Ile Gln Asp Gln Ala Lys His Met Gly Val Met Ala Gly Asp
220          340          345          350
221 Ile Tyr Ser Val Phe Arg Asn Ala Ala Ser Phe Lys Glu Val Ser Asp
222          355          360          365
223 Ser Leu Leu Thr Ser Ser Lys Gly Gln Leu Gln Lys Met Lys Glu Ser
224          370          375          380
225 Leu Asp Asp Val Met Asp Tyr Leu Val Asn Asn Thr Pro Leu Asn Trp
226 385          390          395          400
227 Leu Val Gly Pro Phe Tyr Pro Gln Leu Thr Glu Ser Gln Asn Ala Gln
228          405          410          415
229 Asp Gln Gly Ala Glu Met Asp Lys Ser Ser Gln Glu Thr Gln Arg Ser
230          420          425          430
231 Glu His Lys Thr His
232          435
235 <210> SEQ ID NO: 6
236 <211> LENGTH: 31

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RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/973,322

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TIME: 15:33:49

Input Set : A:\SEQLISTDYOU17001CPl.TXT

Output Set: N:\CRF3\10302001\I973322.raw

237 <212> TYPE: PRT
 238 <213> ORGANISM: Artificial Sequence
 240 <220> FEATURE:
 241 <223> OTHER INFORMATION: branched peptide containing residues 5-27 of HCV
 242 core protein
 244 <221> NAME/KEY: VARIANT
 245 <222> LOCATION: (1)...(31)
 246 <223> OTHER INFORMATION: Xaa = Ala or Pro at position 1, and Ile or Asn at
 247 position 12
 249 <400> SEQUENCE: 6
 W--> 250 Xaa Lys Pro Gln Arg Lys Thr Lys Arg Asn Thr Xaa Arg Arg Pro Gln
 251 1 5 10 15
 252 Asp Val Lys Phe Pro Gly Gly Lys Lys Lys Lys Lys Lys Ala
 253 20 25 30
 256 <210> SEQ ID NO: 7
 257 <211> LENGTH: 11
 258 <212> TYPE: DNA
 259 <213> ORGANISM: Artificial Sequence
 261 <220> FEATURE:
 262 <223> OTHER INFORMATION: oligonucleotides used to construct HCV core
 263 protein deletion plasmids
 265 <400> SEQUENCE: 7
 266 gctgagatct a 11
 268 <210> SEQ ID NO: 8
 269 <211> LENGTH: 29
 270 <212> TYPE: DNA
 271 <213> ORGANISM: Artificial Sequence
 273 <220> FEATURE:
 274 <223> OTHER INFORMATION: oligonucleotides used to construct HCV core
 275 protein deletion plasmids
 277 <400> SEQUENCE: 8
 278 gtaaccttcc tggttgctct tgagatcta 29
 280 <210> SEQ ID NO: 9
 281 <211> LENGTH: 17
 282 <212> TYPE: DNA
 283 <213> ORGANISM: Artificial Sequence
 285 <220> FEATURE:
 286 <223> OTHER INFORMATION: oligonucleotides used to construct HCV core
 287 protein deletion plasmids
 289 <400> SEQUENCE: 9
 290 gtaacctttg agatcta 17
 292 <210> SEQ ID NO: 10
 293 <211> LENGTH: 18
 294 <212> TYPE: DNA
 295 <213> ORGANISM: Artificial Sequence
 297 <220> FEATURE:
 298 <223> OTHER INFORMATION: oligonucleotides used to construct HCV core
 299 protein deletion plasmids
 301 <400> SEQUENCE: 10

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/973,322

DATE: 10/30/2001

TIME: 15:33:50

Input Set : A:\SEQLISTDYOU17001CP1.TXT

Output Set: N:\CRF3\10302001\I973322.raw

L:12 M:270 C: Current Application Number differs, Replaced Current Application No
L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:140 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4
L:164 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4
L:183 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5
L:250 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6